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What is claimed is:

1. A plant expression cassette, which comprises
a glutamine synthetase gene coding sequence operably
linked to a promoter.

2. The expression cassette of claim 1, wherein
the glutamine synthetase coding sequence is from a
gymnosperm.

10 3. The expression cassette of claim 2, wherein
the glutamine synthetase coding sequence is from the
genus *Pinus*.

15 4. The expression cassette of claim 3, wherein
the glutamate synthetase coding sequence is from *Pinus*
sylvestris.

20 5. The expression cassette of claim 2, in which
the promoter is the cauliflower mosaic virus 35S
promoter.

25 6. The expression cassette of claim 5, which
further comprises the NOS terminator sequence operably
linked to the glutamine synthetase coding sequence.

7. The expression cassette of claim 1, which is
30 contains a nucleic acid sequence selected from the group
consisting of:

- A.) a nucleic acid sequence that is at least
70% identical to Genbank Accession No. X69822;
- B.) a nucleic acid sequence that encodes a
protein that is at least 70% similar to Genbank Accession
No. X69822;

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C.) a nucleic acid sequence that hybridizes to Genbank Accession No. X69822 at moderate stringency; and
D.) a nucleic acid sequence that is Genbank Accession No. X69822.

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8. A vector, comprising the expression cassette of claim 1.

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9. The vector of claim 8, which is an Agrobacterium binary vector.

10. The vector of claim 9, wherein the vector is pBIN19.

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11. The vector of claim 10, which further comprises the neomycin phosphotransferase II coding sequence.

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12. A method of producing a plant with improved nitrogen metabolism by transforming *in vitro* said plant with the expression cassette of claim 1.

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13. The method of claim 12, wherein the plant is a woody perennial.

14. The method of claim 13, wherein the plant is in the family Salicaceae.

15. The method of claim 14, wherein the plant is in the genus *Populus*.

16. The method of claim 15, wherein the plant is the hybrid *Populus tremula* X *P. alba*.

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17. The method of claim 16, wherein the plant
is clone INRA 717 1-B4 of hybrid *Populus tremula X P.*
alba.

5 18. The method of claim 12, wherein the
transformation step uses the *Agrobacterium tumifaciens*
method.

10 19. The method of claim 13, wherein the
transformation step further uses the vector of claim 9.

20. A transgenic plant produced by the method
of claim 12.

15 21. A reproductive unit from the transgenic
plant of claim 15.

22. A cell from the transgenic plant of claim

21.

20 23. A transgenic plant with an improved
nitrogen metabolism, which is a woody perennial and
comprises at least one transgene that comprises the
coding sequence of a glutamine synthetase gene.

25 24. The transgenic plant of claim 23, wherein
the glutamine synthetase gene is from a gymnosperm.

30 25. The transgenic plant of claim 24, wherein
the glutamine synthetase genes is from *Pinus sylvestris*.

26. The transgenic plant of claim 25, wherein
the glutamine synthetase coding sequence is Genbank
Accession No. X69822.

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27. The transgenic plant of claim 17, which is from the family Salicaceae.

28. The transgenic plant of claim 23, which is 5 from the genus *Populus*.

29. The transgenic plant of claim 28, which is a hybrid of *Populus tremula* X *Populus alba*.

10 30. The transgenic plant of claim 29, which is clone INRA 717 1-B4 of the hybrid *Populus tremula* X *Populus alba*.

15 31. A reproductive unit from the transgenic plant of claim 23.

20 32. A transgenic plant, which is a woody perennial, and exhibits a growth rate that is statistically significantly greater at the P=0.05 level than that of equivalent untransformed plants.

25 33. The transgenic plant of claim 32, which additionally exhibits a protein concentration in gram per gram fresh weight in the mature leaves that is statistically significantly greater at the P=0.05 level than that of mature leaves in equivalent untransformed plants.

30 34. The transgenic plant of claim 33, which additionally exhibits a chlorophyll concentration in gram per gram fresh weight in the mature leaves that is statistically significantly greater at the P=0.05 level than that of mature leaves in equivalent untransformed plants.

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35. The transgenic plant of claim 34, which
additionally exhibits a mature leaf area in cm² per leaf
that is statistically significantly greater at the P=0.05
level than that of mature leaves in equivalent
5 untransformed plants.

36. The transgenic plant of claim 32, which is
from the family Salicaceae.

10 37. The transgenic plant of claim 36, which is
from the genus *Populus*.

38. The transgenic plant of claim 37, which is
a hybrid of *Populus tremula* X *Populus alba*.

15 39. The transgenic plant of claim 38, which is
clone INRA 717 1-B4 of the hybrid *Populus tremula* X
Populus alba.

20 40. A reproductive unit from the transgenic
plant of claim 32.